



## **Re-approaching new stemmatics**

### **Choice of relationship revealing readings for cladistic analysis.**

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# Re-approaching new stemmatics: Choice of relationship revealing readings for cladistic analysis.

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## AIM

This paper presents preliminary results of my research in the methodological field of computer-assisted stemmatics. It explores the possibilities of applying phylogenetic systematics for textual traditions, as well as discusses the controversies regarding the methodological principles within the field of new stemmatics, such as choice of relationship revealing readings. Additionally, it presents the results of the experiments I have conducted employing the PHYLIP package — a free package of programs for inferring phylogenies, developed by Felsenstein (2005) — aimed to assess an influence of a sample size and types of variants on the results of cladistic analysis. The oldest manuscripts of "Hrómundar saga Gripssonar" — a post-medieval Icelandic saga preserved in 36 manuscripts — served as a case study for the second part of my presentation.

## METHODS

Similarities between theoretical assumptions behind cladistics and stemmatology have been explicitly presented by Howe, Barbrook, Mooney and Robinson (2004) in the second volume of "Studies in Stemmatology". An application of computer-assisted methods, originating from phylogenetics, to answer the questions of textual criticism, has been recognized in an academic discourse as a powerful tool in revealing manuscripts' filiation. Yet, there is a disagreement regarding the fundamental question: what kind of textual variation can, or should, be used for analysis? Salemans (1996) suggested a set of strictly systematized classification of parsimony informative variants, while Robinson (1996) has claimed that all types of variants should be analyzed, including linguistic variants.

Another question that arose recently is a role of small samples in the tree-building process, as discussed by Hall and Parsons (2013). It seems obvious that philologists for centuries used some sort of sampling to reveal manuscript filiation, however they usually did not discuss their sampling procedure, nor publish underlying samples. This attitude does not belong to the age of open scholarship, which requires access to data to allow replication of experiments.

This paper takes an experimental approach towards the mentioned problems, thus a number of tests have been conducted to support the claims made by the author, discussed below in the "Main Findings" section.

## RESEARCH QUESTIONS

The experiments I have conducted sought answers for the following questions:

- How does linguistic variation influence the manuscripts' filiation?
- How to choose a relationship revealing variants?
- Are complete transcriptions of all witnesses necessary to conduct a computer-assisted analysis?
- If not, how small can a sample be? Can analysis be based only on *loci critici*?

## MAIN FINDINGS AND UNDERLYING WORK

In my paper I present the results of the experiments I have conducted with use of Pars — a general parsimony program — and DrawTree and Consense — tree-plotting programs, included in the PHYLIP package. The aim of the experiments was to assess the influence of linguistic and minor variants on the results of a cladistics analysis. Additionally I conducted experiments, which aimed to examine an influence of a sample size on the results. For that purpose I employed a sequential analysis for all the characters I collected from the entire saga. The results of each experiment were plotted into Consense software, in order to achieve a consensus tree on which the stemma can be based.

The results of my experiments suggest that cladistics can be employed in traditional textual criticism, and that computer assisted methods improve efficiency of the analysis by decreasing the time necessary for traditional data interpretation. I claim that an input dataset can be based only on traditional *loci critici*, and the achieved results are as equally valid as the ones based on complete transcriptions, which include all sorts of

variants. Moreover, the presence of linguistic variants seemed to introduce noise to the analysis.

## RELEVANCE

My paper aims to present possibilities given to a textual critic by an application of tools developed within evolutionary biology. Even though the discussion on applications of cladistics in philological research has been present in the academic discourse for around thirty years now, as presented by Salemans (1987), the computer-assisted methods seem to still face resistance from traditional philologists, most recently expressed by Trovato (2014). The possible reasons for this lack of trust in cladistics will be briefly addressed in this paper.

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